

humanVR1 gene with translation of open reading frame

**Input file FchrB87a6.seq; Output File FchrB87a6.trn
Sequence length 3909**

M	K	K	W	S	S	T	D	L	G	T	A	A	D	P	L	Q	K	18		
GCAAGG	ATG	AAG	AAA	TGG	AGC	AGC	ACA	GAC	TTG	GGG	ACA	GCT	GCG	GAC	CCA	CTC	CAA	AAG	54	
D	T	C	P	D	P	L	D	G	D	P	N	S	R	P	P	P	A	K	38	
GAC	ACC	TGC	CCA	GAC	CCC	CTG	GAT	GGA	GAC	CCT	AAC	TCC	AGG	CCA	CCT	CCA	GCC	AAG	CCC	114
Q	L	P	T	A	K	S	R	T	R	L	F	G	K	G	D	S	E	E	A	58
CAG	CTC	CCC	ACG	GCC	AAG	AGC	CGC	ACC	CGG	CTC	TTT	GGG	AAG	GGT	GAC	TCG	GAG	GAG	GCT	174
F	P	V	D	C	P	H	E	E	G	E	L	D	S	C	P	T	I	T	V	78
TTC	CCG	GTG	GAT	TGC	CCC	CAC	GAG	GAA	GGT	GAG	TTG	GAC	TCC	TGC	CCG	ACC	ATC	ACA	GTC	234
S	P	V	I	T	I	Q	R	P	G	D	G	P	T	G	A	R	L	L	S	98
AGC	CCT	GTT	ATC	ACC	ATC	CAG	AGG	CCA	GGA	GAC	GGC	CCC	ACC	GGT	GCC	AGG	CTG	CTG	TCC	294
Q	D	S	V	A	A	S	T	E	K	T	L	R	L	Y	D	R	R	S	I	118
CAG	GAC	TCT	GTC	GCC	GCC	AGC	ACC	GAG	AAG	ACC	CTC	AGG	CTC	TAT	GAT	CGC	AGG	AGT	ATC	354
F	E	A	V	A	Q	N	N	C	Q	D	L	E	S	L	L	L	F	L	Q	138
TTT	GAA	GCC	GTT	GCT	CAG	AAT	AAC	TGC	CAG	GAT	CTG	GAG	AGC	CTG	CTG	CTC	TTC	CTG	CAG	414

FIGURE 1A

K	S	K	K	H	L	T	D	N	E	F	K	D	P	E	T	G	K'	T	C	158
AAG	AGC	AAG	AAG	CAC	CTC	ACA	GAC	AAC	GAG	TTC	AAA	GAC	CCT	GAG	ACA	GGG	AAG	ACC	TGT	474
L	L	K	A	M	L	N	L	H	D	G	Q	N	T	T	I	P	L	L	L	178
CTG	CTG	AAA	GCC	ATG	CTC	AAC	CTG	CAC	GAC	GGA	CAG	AAC	ACC	ACC	ATC	CCC	CTG	CTC	CTG	534
E	I	A	R	Q	T	D	S	L	K	E	L	V	N	A	S	Y	T	D	S	198
GAG	ATC	GCG	CGG	CAA	ACG	GAC	AGC	CTG	AAG	GAG	CTT	GTC	AAC	GCC	AGC	TAC	ACG	GAC	AGC	594
Y	Y	K	G	Q	T	A	L	H	I	A	I	E	R	R	N	M	A	L	V	218
TAC	TAC	AAG	GGC	CAG	ACA	GCA	CTG	CAC	ATC	GCC	ATC	GAG	AGA	CGC	AAC	ATG	GCC	CTG	GTG	654
T	L	L	V	E	N	G	A	D	V	Q	A	A	A	H	G	D	F	F	K	238
ACC	CTC	CTG	GTG	GAG	AAC	GGA	GCA	GAC	GTC	CAG	GCT	GCG	GCC	CAT	GGG	GAC	TTC	TTT	AAG	714
K	T	K	G	R	P	G	F	Y	F	G	E	L	P	L	S	L	A	A	C	258
AAA	ACC	AAA	GGG	CGG	CCT	GGA	TTC	TAC	TTC	GGT	GAA	CTG	CCC	CTG	TCC	CTG	GCC	GCG	TGC	774
T	N	Q	L	G	I	V	K	F	L	L	Q	N	S	W	Q	T	A	D	I	278
ACC	AAC	CAG	CTG	GGC	ATC	GTG	AAG	TTC	CTG	CTG	CAG	AAC	TCC	TGG	CAG	ACG	GCC	GAC	ATC	834
S	A	R	D	S	V	G	N	T	V	L	H	A	L	V	E	V	A	D	N	298
AGC	GCC	AGG	GAC	TCG	GTG	GGC	AAC	ACG	GTG	CTG	CAC	GCC	CTG	GTG	GAG	GTG	GCC	GAC	AAC	894
T	A	D	N	T	K	F	V	T	S	M	Y	N	E	I	L	M	L	G	A	318
ACG	GCC	GAC	AAC	ACG	AAG	TTT	GTG	ACG	AGC	ATG	TAC	AAT	GAG	ATT	CTG	ATG	CTG	GGG	GCC	954
K	L	H	P	T	L	K	L	E	E	L	T	N	K	K	G	M	T	P	L	338
AAA	CTG	CAC	CCG	ACG	CTG	AAG	CTG	GAG	GAG	CTC	ACC	AAC	AAG	AAG	GGA	ATG	ACG	CCG	CTG	1014
A	L	A	A	G	T	G	K	I	G	V	L	A	Y	I	L	Q	R	E	I	358
GCT	CTG	GCA	GCT	GGG	ACC	GGG	AAG	ATC	GGG	GTC	TTG	GCC	TAT	ATT	CTC	CAG	CGG	GAG	ATC	1074
Q	E	P	E	C	R	H	L	S	R	K	F	T	E	W	A	Y	G	P	V	378
CAG	GAG	CCC	GAG	TGC	AGG	CAC	CTG	TCC	AGG	AAG	TTC	ACC	GAG	TGG	GCC	TAC	GGG	CCC	GTG	1134
H	S	S	L	Y	D	L	S	C	I	D	T	C	E	K	N	S	V	L	E	398
CAC	TCC	TCG	CTG	TAC	GAC	CTG	TCC	TGC	ATC	GAC	ACC	TGC	GAG	AAG	AAC	TCG	GTG	CTG	GAG	1194
V	I	A	Y	S	S	E	T	P	N	R	H	D	M	L	L	V	E	P	418	
GTG	ATC	GCC	TAC	AGC	AGC	AGC	GAG	ACC	CCT	AAT	CGC	CAC	GAC	ATG	CTC	TTG	GTG	GAG	CCG	1254
L	N	R	L	L	Q	D	K	W	D	R	F	V	K	R	I	F	Y	F	N	438
CTG	AAC	CGA	CTC	CTG	CAG	GAC	AAG	TGG	GAC	AGA	TTC	GTC	AAG	CGC	ATC	TTC	TAC	TTC	AAC	1314
F	L	V	Y	C	L	Y	M	I	I	F	T	M	A	A	Y	Y	R	P	V	458
TTC	CTG	GTC	TAC	TGC	CTG	TAC	ATG	ATC	ATC	TTC	ACC	ATG	GCT	GCC	TAC	TAC	AGG	CCC	GTG	1374
D	G	L	P	P	F	K	M	E	K	I	G	D	Y	F	R	V	T	G	E	478
GAT	GGC	TTG	CCT	CCC	TTT	AAG	ATG	GAA	AAA	ATT	GGA	GAC	TAT	TTC	CGA	GTT	ACT	GGA	GAG	1434
I	L	S	V	L	G	G	V	Y	F	F	F	R	G	I	Q	Y	F	L	Q	498
ATC	CTG	TCT	GTG	TTA	GGA	GGA	GTC	TAC	TTC	TTT	TTC	CGA	GGG	ATT	CAG	TAT	TTC	CTG	CAG	1494

FIGURE 1 (cont'd) B

R	R	P	S	M	K	T	L	F	V	D	S	Y	S	E	M	L	F	F	L	518
AGG	CGG	CCG	TCG	ATG	AAG	ACC	CTG	TTT	GTG	GAC	AGC	TAC	AGT	GAG	ATG	CTT	TTC	TTT	CTG	1554
Q	S	L	F	M	L	A	T	V	V	L	Y	F	S	H	L	K	E	Y	V	538
CAG	TCA	CTG	TTC	ATG	CTG	GCC	ACC	GTG	GTG	CTG	TAC	TTC	AGC	CAC	CTC	AAG	GAG	TAT	GTG	1614
A	S	M	V	F	S	L	A	L	G	W	T	N	M	L	Y	Y	T	R	G	558
GCT	TCC	ATG	GTA	TTC	TCC	CTG	GCC	TTG	GGC	TGG	ACC	AAC	ATG	CTC	TAC	TAC	ACC	CGC	GGT	1674
F	Q	Q	M	G	I	Y	A	V	M	I	E	K	M	I	L	R	D	L	C	578
TTC	CAG	CAG	ATG	GGC	ATC	TAT	GCC	GTC	ATG	ATA	GAG	AAG	ATG	ATC	CTG	AGA	GAC	CTG	TGC	1734
R	F	M	F	V	Y	I	V	F	L	F	G	F	S	T	A	V	V	T	L	598
CGT	TTC	ATG	TTT	GTC	TAC	ATC	GTC	TTC	TTG	GGG	TTT	TCC	ACA	GCG	GTG	GTG	ACG	CTG	1794	
I	E	D	G	K	N	D	S	L	P	S	E	S	T	S	H	R	W	R	G	618
ATT	GAA	GAC	GGG	AAG	AAT	GAC	TCC	CTG	CCG	TCT	GAG	TCC	ACG	TCG	CAC	AGG	TGG	CGG	GGG	1854
P	A	C	R	P	P	D	S	S	Y	N	S	L	Y	S	T	C	L	E	L	638
CCT	GCC	TGC	AGG	CCC	CCC	GAT	AGC	TCC	TAC	AAC	AGC	CTG	TAC	TCC	ACC	TGC	CTG	GAG	CTG	1914
F	K	F	T	I	G	M	G	D	L	E	F	T	E	N	Y	-D	F	K	A	658
TTC	AAG	TTC	ACC	ATC	GGC	ATG	GGC	GAC	CTG	GAG	TTC	ACT	GAG	AAC	TAT	GAC	TTC	AAG	GCT	1974
V	F	I	I	L	L	L	A	Y	V	I	L	T	Y	I	L	L	L	N	M	678
GTC	TTC	ATC	ATC	CTG	CTG	GCC	TAT	GTA	ATT	CTC	ACC	TAC	ATC	CTC	CTG	CTC	AAC	ATG	2034	
L	I	A	L	M	G	E	T	V	N	K	I	A	Q	E	S	K	N	I	W	698
CTC	ATC	GCC	CTC	ATG	GGT	GAG	ACT	GTC	AAC	AAG	ATC	GCA	CAG	GAG	AGC	AAG	AAC	ATC	TGG	2094
K	L	Q	R	A	I	T	I	L	D	T	E	K	S	F	L	K	C	M	R	718
AAG	CTG	CAG	AGA	GCC	ATC	ACC	ATC	CTG	GAC	ACG	GAG	AAG	AGC	TTC	CTT	AAG	TGC	ATG	AGG	2154
K	A	F	R	S	G	K	L	L	Q	V	G	Y	T	P	D	G	K	D	D	738
AAG	GCC	TTC	CGC	TCA	GGC	AAG	CTG	CTG	CAG	GTG	GGG	TAC	ACA	CCT	GAT	GGC	AAG	GAC	GAC	2214
Y	R	W	C	F	R	V	D	E	V	N	W	T	T	W	N	T	N	V	G	758
TAC	CGG	TGG	TGC	TTC	AGG	GTG	GAC	GAG	GTG	AAC	TGG	ACC	ACC	TGG	AAC	ACC	AAC	GTG	GGC	2274
I	I	N	E	D	P	G	N	C	E	G	V	K	R	T	L	S	F	S	L	778
ATC	ATC	AAC	GAA	GAC	CCG	GGC	AAC	TGT	GAG	GGC	GTC	AAG	CGC	ACC	CTG	AGC	TTC	TCC	CTG	2334
R	S	S	R	V	S	G	R	H	W	K	N	F	A	L	V	P	L	L	R	798
CGG	TCA	AGC	AGA	GTY	TCA	GGC	ACA	CAC	TGG	AAG	AAC	TTC	GGC	CTG	GTC	CCC	CTT	TTA	AGA	2394
E	A	S	A	R	D	R	Q	S	A	Q	P	E	E	V	Y	L	R	Q	F	818
GAG	GCA	AGT	GCT	CGA	GAT	AGG	CAG	TCT	GCT	CAG	CCC	GAG	GAA	GTT	TAT	CTG	CGA	CAG	TTT	2454
S	G	S	L	K	P	E	D	A	E	V	F	K	S	P	A	A	S	G	E	838
TCA	GGG	TCT	CTG	AAG	CCA	GAG	GAC	GCT	GAG	GTC	TTC	AAG	AGT	CCT	GCC	GCT	TCC	GGG	GAG	2514
K	*																			840
AAG	TGA																			2520

FIGURE 1 (cont'd) C

GGACGTCACCGAGACAGCACTGTCAACACTGGCCTTAGGAGACCCGTTGCCACGGGGGCTGCTGAGGGAACACCAG
TGCTCTGTCAGCAGCCTGGCCTGGTCTGTGCCTGCCAGCATGTTCCAAATCTGTGCTGGACAAGCTGTGGGAAGCGT
TCTTGGAAAGCATGGGAGTGATGTACATCCAACCGTCACTGTCCCCAAGTGAATCTCTAACAGACTTCAGGTTTTA
CTCACTTTACTAAAAAAAAAAAAAGGGCGGCCGCTTA

FIGURE 1 (cont'd) D

humanVR1 gene with translation of open reading frame

Input file Fchrb87a6.seq; Output File Fchrb87a6.tra
 Sequence length 3909

GTGAGCGCAACGCACTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGCAA
 CGCAC TGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGAACGCACTGCGG
 GCAGTGAGCGAACGCACTTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGC
 GCAACGCACTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGAACGCACT
 GCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTGAGCGAACGCACTGCGGGCAGTG
 AGCGAACGCACTGCGGGCAGTGAGCGAACGCACTTGAGCTTAATGTGAGTTAGCTCACTCATTAGGCACCCAGGCTTACAC
 TTTATGCTTCGGCTCGTATGTTGTGGAATTGTGAGCGATAACAATTTCACACAGGAAACAGCTATGACCATGATT
 ACGCCAAGCTCTAATACGACTCACTATAGGAAAGCTGGTACGCCCTGAGGTACCGGTCCGGAATTCCCGGGTCGACCC
 ACGCGTCCGAAAACACACCTCTGTGCTGGAAAGACTGTGCAATGGCACAGCCGAGAGCTTGGTTGGAGGTTGAA
 GTGCTCTGGGAGAATTCTGAGATCATCCTCAGAAAAGCCTGCCCTGGTGTCTACCAGAAAACGTCTCCAATCAC
 CCAGAAAAGCTGTCCACAGTAGTCCCCCTTATCCACGGGTGTCACTTCCATGGGTTAGTTATTGCGGTCAACCAC
 GGTCTGCCAATATTAAATGGAAAATTCTTCAAACAGTTCCAAGTTTCCCTGTGCATTGTTCTGAGCAGTGTGATGA
 AGAGTCTCTGCCGTGCCATCTGGGATGCAAACCGTCCCTGTGCCCCCACGTCCAGGCCGTAGATGCTCCCCGCCGGTC
 AGTCACCTAGTCGTCAAGATGCCCGTCTGGTATCACAGTGCTCTGTTAGGTTGCACACTGGCCACAGAGGATCCA

M	K	K	W	S	S	T	D	L	G	T	A	A	D	P	L	Q	K	18
GCAAGG	ATG	AAG	AAA	TGG	AGC	AGC	ACA	GAC	TTG	GGG	ACA	GCT	GCG	GAC	CCA	CTC	CAA	54
D	T	C	P	D	P	L	D	G	D	P	N	S	R	P	P	P	A	38
GAC	ACC	TGC	CCA	GAC	CCC	CTG	GAT	GGA	GAC	CCT	AAC	TCC	AGG	CCA	CCT	CCA	GCC	114
Q	L	P	T	A	K	S	R	T	R	L	F	G	K	G	D	S	E	58
CAG	CTC	CCC	ACG	GCC	AAG	AGC	CGC	ACC	CGG	CTC	TTT	GGG	AAG	GGT	GAC	TCG	GAG	174
F	P	V	D	C	P	H	E	E	G	E	L	D	S	C	P	T	I	78
TTC	CCT	GTC	ATG	CGA	CGG	CGG	CGC	CGC	CGC	CGC	TTC	GTC	TTC	TTC	CGC	ACC	ATC	234
S	P	V	I	T	I	Q	R	P	G	D	G	P	T	G	A	R	L	98
AGC	CCT	GTT	ATC	ACC	ATC	CAG	AGG	CCA	GGA	GAC	GGC	CCC	ACC	GGT	GCC	AGG	CTG	294
Q	D	S	V	A	A	S	T	E	K	T	L	R	L	Y	D	R	R	118
CAG	GAC	TCT	GTC	GCC	GCC	AGC	ACC	GAG	AAG	ACC	CTC	AGG	CTC	TAT	GAT	CGC	AGG	354
F	E	A	V	A	Q	N	N	C	Q	D	L	E	S	L	L	L	F	138
TTT	GAA	GCC	GTT	GCT	CAG	AAT	AAC	TGC	CAG	GAT	CTG	GAG	AGC	CTG	CTG	CTC	CTG	414

FIGURE 1A

K S K K H L T D N E F K D P E T G K' T C	158
AAG AGC AAG AAG CAC CTC ACA GAC AAC GAG TTC AAA GAC CCT GAG ACA GGG AAG ACC TGT	474
L L K A M L N L H D G Q N T T I P L L L	178
CTG CTG AAA GCC ATG CTC AAC CTG CAC GAC GGA CAG AAC ACC ACC ATC CCC CTG CTC CTG	534
E I A R Q T D S L K E L V N A S Y T D S	198
GAG ATC GCG CGG CAA ACG GAC AGC CTG AAG GAG CTT GTC AAC GCC AGC TAC ACG GAC AGC	594
Y Y K G Q T A L H I A I E R R N M A L V	218
TAC TAC AAG GGC CAG ACA GCA CTG CAC ATC GCC ATC GAG AGA CGC AAC ATG GCC CTG GTG	654
T L L V E N G A D V Q A A A H G D F F K	238
ACC CTC CTG GTG GAG AAC GGA GCA GAC GTC CAG GCT GCG GCC CAT GGG GAC TTC TTT AAG	714
K T K G R P G F Y F G E L P L S L A A C	258
AAA ACC AAA GGG CGG CCT GGA TTC TAC TTC GGT GAA CTG CCC CTG TCC CTG GCC GCG TGC	774
T N Q L G I V K F L L Q N S W Q T A D I	278
ACC AAC CAG CTG GGC ATC GTG AAG TTC CTG CAG AAC TCC TGG CAG ACG GCC GAC ATC	834
S A R D S V G N T V L H A L V E V A D N	298
AGC GCC AGG GAC TCG GTG GGC AAC ACG GTG CTG CAC GCC CTG GTG GAG GTG GCC GAC AAC	894
T A D N T K F V T S M Y N E I L M L G A	318
ACG GCC GAC AAC ACG AAG TTT GTG ACG AGC ATG TAC AAT GAG ATT CTG ATG CTG GGG GCC	954
K L H P T L K L E E L T N K K G M T P L	338
AAA CTG CAC CCG ACG CTG AAG CTG GAG CTC ACC AAC AAG AAG GGA ATG ACG CCG CTG	1014
A L A A G T G K I G V L A Y I L Q R E I	358
GCT CTG GCA GCT GGG ACC GGG AAG ATC GGG GTC TTG GCC TAT ATT CTC CAG CGG GAG ATC	1074
Q E P E C R H L S R K F T E W A Y G P V	378
CAG GAG CCC GAG TGC AGG CAC CTG TCC AGG AAG TTC ACC GAG TGG GCC TAC GGG CCC GTG	1134
H S S L Y D L S C I D T C E K N S V L E	398
CAC TCC TCG CTG TAC GAC CTG TCC TGC ATC GAC ACC TGC GAG AAG AAC TCG GTG CTG GAG	1194
V I A Y S S S E T P N R H D M L L V E P	418
GTC ATC GCC TAC AGC AGC GAG ACC CCT AAT CGC CAC GAC ATG CTC TTG GTG GAG CCG	1254
L N K L L Q D K W D R F V K K I F Y F N	438
CTG AAC CGA CTC CTG CAG GAC AAG TGG GAC AGA TTC GTC AAG CGC ATC TTC TAC TTC AAC	1314
F L V Y C L Y M I I F T M A A Y Y R P V	458
TTC CTG GTC-TAC TGC CTG TAC ATG ATC ATC TTC ACC ATG GCT GCC TAC TAC AGG CCC GTG	1374
D G L P P F K M E K I G D Y F R V T G E	478
GAT GGC TTG CCT CCC TTT AAG ATG GAA AAA ATT GGA GAC TAT TTC CGA GTT ACT GGA GAG	1434
I L S V L G G V Y F F F R G I Q Y F L Q	498
ATC CTG TCT GTG TTA GGA GGA GTC TAC TTC TTG CGA GGG ATT CAG TAT TTC CTG CAG	1494

FIGURE 1

R R P S M K T L F V D S Y S E M L F . . . F L	518
AGG CGG CCG TCG ATG AAG ACC CTG TTT GTG GAC AGC TAC AGT GAG ATG CTT TTC TTT CTG	1554
Q S L F M L A T V V L Y F S H L K E Y V	538
CAG TCA CTG TTC ATG CTG GCC ACC GTG GTG CTG TAC TTC AGC CAC CTC AAG GAG TAT GTG	1614
A S M V F S L A L G W T N M L Y Y T R G	558
GCT TCC ATG GTA TTC TCC CTG GCC TTG GGC TGG ACC AAC ATG CTC TAC TAC ACC CGC GGT	1674
F Q Q M G I Y A V M I E K M I L R D L C	578
TTC CAG CAG ATG GGC ATC TAT GCC GTC ATG ATA GAG AAG ATG ATC CTG AGA GAC CTG TGC	1734
R F M F V Y I V F L F G F S T A V V T L	598
CGT TTC ATG TTT GTC TAC ATC GTC TTC TTG GGG TTT TCC ACA GCG GTG GTG ACG CTG	1794
I E D G K N D S L P S E S T S H R W R G	618
ATT GAA GAC GGG AAG AAT GAC TCC CTG CCG TCT GAG TCC ACG TCG CAC AGG TGG CGG GGG	1854
P A C R P P D S S Y N S L Y S T C L E L	638
CCT GCC TGC AGG CCC CCC GAT AGC TCC TAC AAC AGC CTG TAC TCC ACC TGC CTG GAG CTG	1914
F K F T I G M G D L E F T E N Y - D F K A	658
TTC AAG TTC ACC ATC GGC ATG GGC GAC CTG GAG TTC ACT GAG AAC TAT GAC TTC AAG GCT	1974
V F I I L L A Y V I L T Y I L L L N M	678
GTC TTC ATC ATC CTG CTG GCC TAT GTA ATT CTC ACC TAC ATC CTC CTG CTC AAC ATG	2034
L I A L M G E T V N K I A Q E S K N I W	698
CTC ATC GCC CTC ATG GGT GAG ACT GTC AAC AAG ATC GCA CAG GAG AGC AAG AAC ATC TGG	2094
K L Q R A I T I L D T E K S F L K C M R	718
AAG CTG CAG AGA GCC ATC ACC ATC CTG GAC ACG GAG AAG AGC TTC CTT AAG TGC ATG AGG	2154
K A F R S G K L L Q V G Y T P D G K D D	738
AAG GCC TTC CGC TCA GGC AAG CTG CTG CAG GTG GGG TAC ACA CCT GAT GGC AAG GAC GAC	2214
Y R W C F R V D E V N W T T W N T N V G	758
TAC CGG TGG TGC TTC AGG GTG GAC GAG GTG AAC TGG ACC ACC TGG AAC ACC AAC GTG GGC	2274
I I N E D P G N C E G V K R T L S F S L	778
ATC ATC AAC GAA GAC CCG GGC AAC TGT GAG GGC GTC AAG CGC ACC CTG AGC TTC TCC CTG	2334
R S S R V S G R H W K N F A L V P L L R	798
CGG TCA ASL ACR CTG TCA GGC AGA CAC TGG AAG AAC TTT GCG CTC CTC CCC CTT TTA AGA	2394
E A S A R D R Q S A Q P E E V Y L R Q F	818
GAG GCA AGT GCT CGA GAT AGG CAG TCT GCT CAG CCC GAG GAA GTT TAT CTG CGA CAG TTT	2454
S G S L K P E D A E V F K S P A A S G E	838
TCA GGG TCT CTG AAG CCA GAG GAC GCT GAG GTC TTC AAG AGT CCT GCT GCT TCC GGG GAG	2514
K *	840
AAG TGA	2520

FIGURE 1c

GGACGTCACGCAGACAGCACTGTCAACACTGGGCCTTAGGAGACCCCGTTGCCACGGGGGCTGCTGAGGGAACACCAAG
TGCTCTGTCAGCAGCCTGGCTGGTCTGTGCCCTGCCAGCATGTTCCAAATCTGTGCTGGACAAGCTGTGGGAAGCGT
TCTTGGAAAGCATGGGAGTGATGTACATCCAACCGTCACTGTCCCCAAGTGAATCTCCTAACAGACTTTCAGGTTTTA
CTCACTTTACTAAAAAAAAAAAAAGGGCGGCCGCTTA

FIGURE 1D